SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying substances which positively influence inflammatory conditions

<130> 1/1179

<140>
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<150> US 60/257,856
<151> 2000-12-22

<160> 8

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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tatatggaat ggatcctgaa ctccttagca tggtaccaag accagtctgt gcagtcttac 180
ttctctttcc tattacagaa aagtatgaag tattcagaac agaagaggaa gaaaaaataa 240
aatctcaggg acaagatgtt acatcatcag tatatttcat gaagcaaaca atcagcaatg 300
cctgtggaac aattggactg attcatgcta ttgcaaacaa taaagacaag atgcactttg 360
aatctggatc aaccttgaaa aaattcctgg aggaatctgt gtcaatgagc cctgaagaac 420

gagccagata cctggagaac tatgatgcca tccgagttac tcatgagacc agtgcccatg 480
aaggtcagac tgaggcacca agtatagatg agaaagtaga tcttcatttt attgcattag 540
ttcatgtaga tgggcatctc tatgaattag atgggcggaa gccatttcca attaaccatg 600
gtgaaactag tgatgaaact ttattagagg atgccataga agtttgcaag aagtttatgg 660
agcgcgaccc tgatgaacta agatttaatg cgattgctct ttctgcagca tagcttgtca 720
ataatggaaa caccaaaaac tgtattattt gcaactaaat tttctctgcc catacactaa 780
ctcaaaaatt ttgatatttt cc 802

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<212> PRT
<213> Homo sapiens

<400> 4

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Asn Gln Phe Leu Lys Gln Leu Gly Leu His Pro Asn Trp Gln Phe Val
             20                  25                  30

Asp Val Tyr Gly Met Asp Pro Glu Leu Leu Ser Met Val Pro Arg Pro
         35                  40                  45

Val Cys Ala Val Leu Leu Leu Phe Pro Ile Thr Glu Lys Tyr Glu Val
     50                  55                  60

Phe Arg Thr Glu Glu Glu Glu Lys Ile Lys Ser Gln Gly Gln Asp Val
 65                  70                  75                  80

Thr Ser Ser Val Tyr Phe Met Lys Gln Thr Ile Ser Asn Ala Cys Gly
                 85                  90                  95

Thr Ile Gly Leu Ile His Ala Ile Ala Asn Asn Lys Asp Lys Met His
            100                 105                 110

Phe Glu Ser Gly Ser Thr Leu Lys Lys Phe Leu Glu Glu Ser Val Ser
        115                 120                 125

Met Ser Pro Glu Glu Arg Ala Arg Tyr Leu Glu Asn Tyr Asp Ala Ile
    130                 135                 140

Arg Val Thr His Glu Thr Ser Ala His Glu Gly Gln Thr Glu Ala Pro
145                 150                 155                 160

Ser Ile Asp Glu Lys Val Asp Leu His Phe Ile Ala Leu Val His Val
                165                 170                 175

Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Lys Pro Phe Pro Ile Asn
            180                 185                 190

His Gly Glu Thr Ser Asp Glu Thr Leu Leu Glu Asp Ala Ile Glu Val
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Cys Lys Lys Phe Met Glu Arg Asp Pro Asp Glu Leu Arg Phe Asn Ala
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<212> DNA
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<220>
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 7
<211> 866
<212> DNA
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gcaaatggtg tggtattagc aactgagaaa aaacagaaat ccattctgta tgatgagcga 180
agtgtacaca aagtagaacc aattaccaag catataggtt tggtgtacag tggcatgggc 240
cccgattaca gagtgcttgt gcacagagct cgaaaactag ctcaacaata ctatcttgtg 300
taccaagaac ccattcctac agctcagctg gtacagagag tagcttctgt gatgcaagaa 360
tatactcagt caggtggtgt tcgtccattt ggagtttctt tacttatttg tggttggaat 420
gagggacgac catatttatt tcagtcagat ccatctggag cttactttgc ctggaaagct 480
acagcaatgg gaaagaacta tgtgaatggg aagactttcc ttgagaaaag atataatgaa 540
gatctggaac ttgaagatgc cattcataca gccatcttaa ccctaaagga aagctttgaa 600
gggcaaatga cagaggataa catagaagtt ggaatctgca atgaagctgg atttaggagg 660
cttactccaa ctgaagttaa ggattacttg gctgccatag cataacaatg aagtgactga 720
aaaatccaga atttcagata atctatctac ttaaacatgt ttaaagtatg ttttgttttg 780
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<210> 8
<211> 234
<212> PRT
<213> Homo sapiens

<400> 8

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Met Ala Glu Arg Gly Tyr Ser Phe Ser Leu Thr Thr Phe Ser Pro Ser
 1               5                  10                  15

Gly Lys Leu Val Gln Ile Glu Tyr Ala Leu Ala Ala Val Ala Gly Gly
            20                  25                  30

Ala Pro Ser Val Gly Ile Lys Ala Ala Asn Gly Val Val Leu Ala Thr
        35                  40                  45

Glu Lys Lys Gln Lys Ser Ile Leu Tyr Asp Glu Arg Ser Val His Lys
    50                  55                  60

Val Glu Pro Ile Thr Lys His Ile Gly Leu Val Tyr Ser Gly Met Gly
65                  70                  75                  80

Pro Asp Tyr Arg Val Leu Val His Arg Ala Arg Lys Leu Ala Gln Gln
                85                  90                  95

Tyr Tyr Leu Val Tyr Gln Glu Pro Ile Pro Thr Ala Gln Leu Val Gln
            100                 105                 110

Arg Val Ala Ser Val Met Gln Glu Tyr Thr Gln Ser Gly Gly Val Arg
        115                 120                 125

Pro Phe Gly Val Ser Leu Leu Ile Cys Gly Trp Asn Glu Gly Arg Pro
    130                 135                 140

Tyr Leu Phe Gln Ser Asp Pro Ser Gly Ala Tyr Phe Ala Trp Lys Ala
145                 150                 155                 160

Thr Ala Met Gly Lys Asn Tyr Val Asn Gly Lys Thr Phe Leu Glu Lys
                165                 170                 175

Arg Tyr Asn Glu Asp Leu Glu Leu Glu Asp Ala Ile His Thr Ala Ile
            180                 185                 190

Leu Thr Leu Lys Glu Ser Phe Glu Gly Gln Met Thr Glu Asp Asn Ile
        195                 200                 205

Glu Val Gly Ile Cys Asn Glu Ala Gly Phe Arg Arg Leu Thr Pro Thr
    210                 215                 220

Glu Val Lys Asp Tyr Leu Ala Ala Ile Ala
225                 230
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